

ORIGINAL RESEARCH ARTICLE

Cancer-testis antigens in gastric adenocarcinoma: Integration of differential expression, clinical associations, survival, and co-expression networks

Supplementary Files

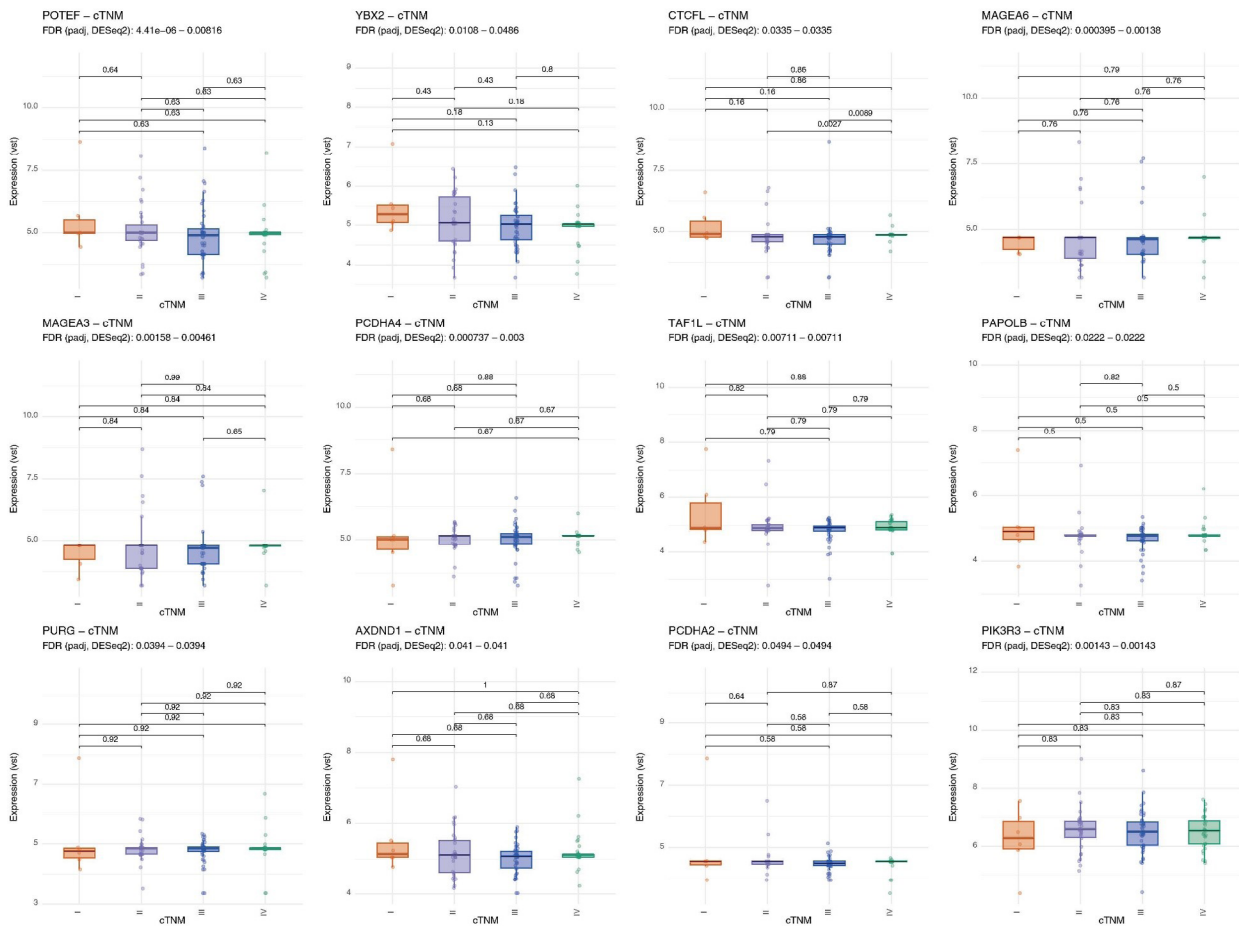


Figure S1. Continued

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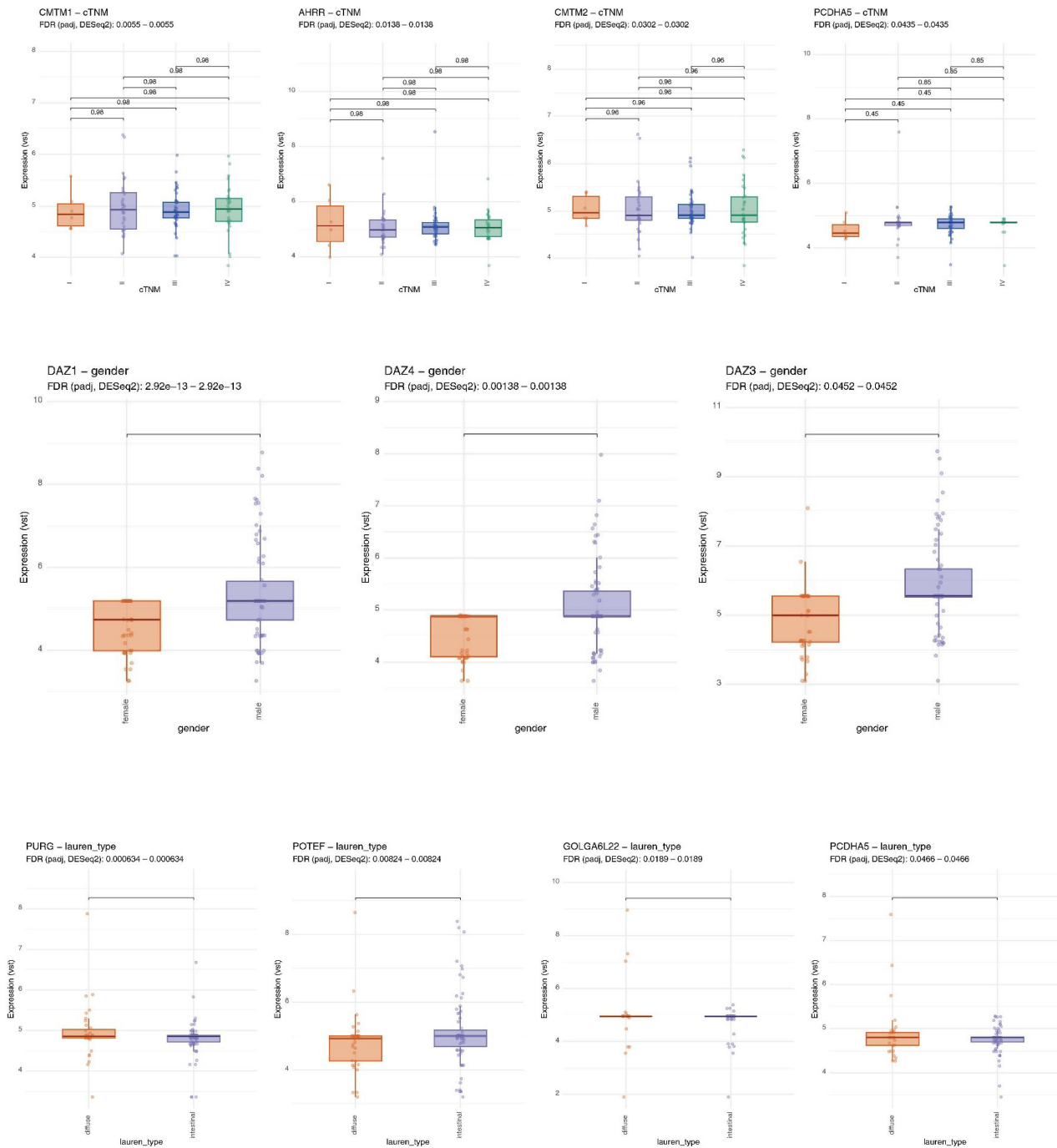


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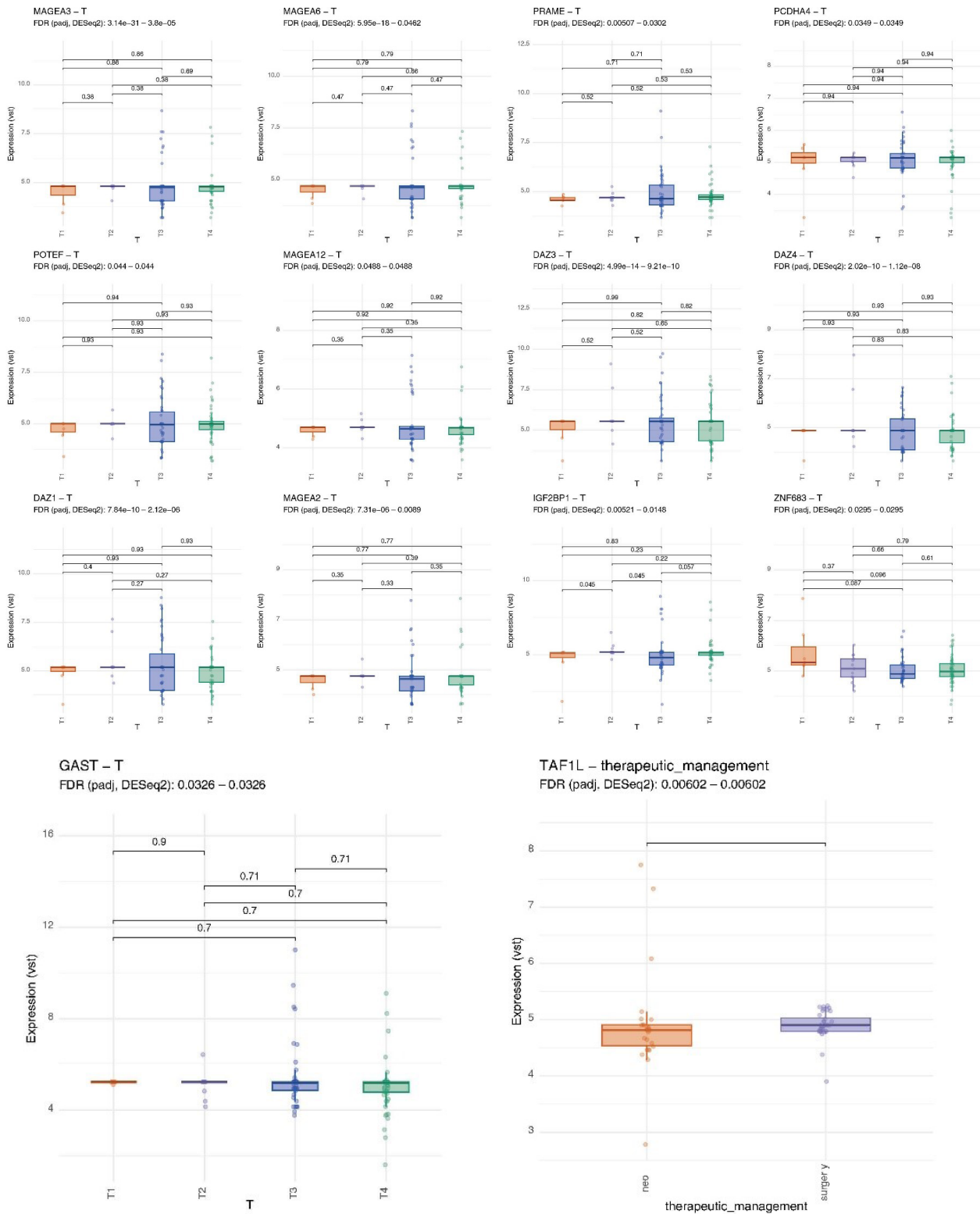


Figure S1. Continued

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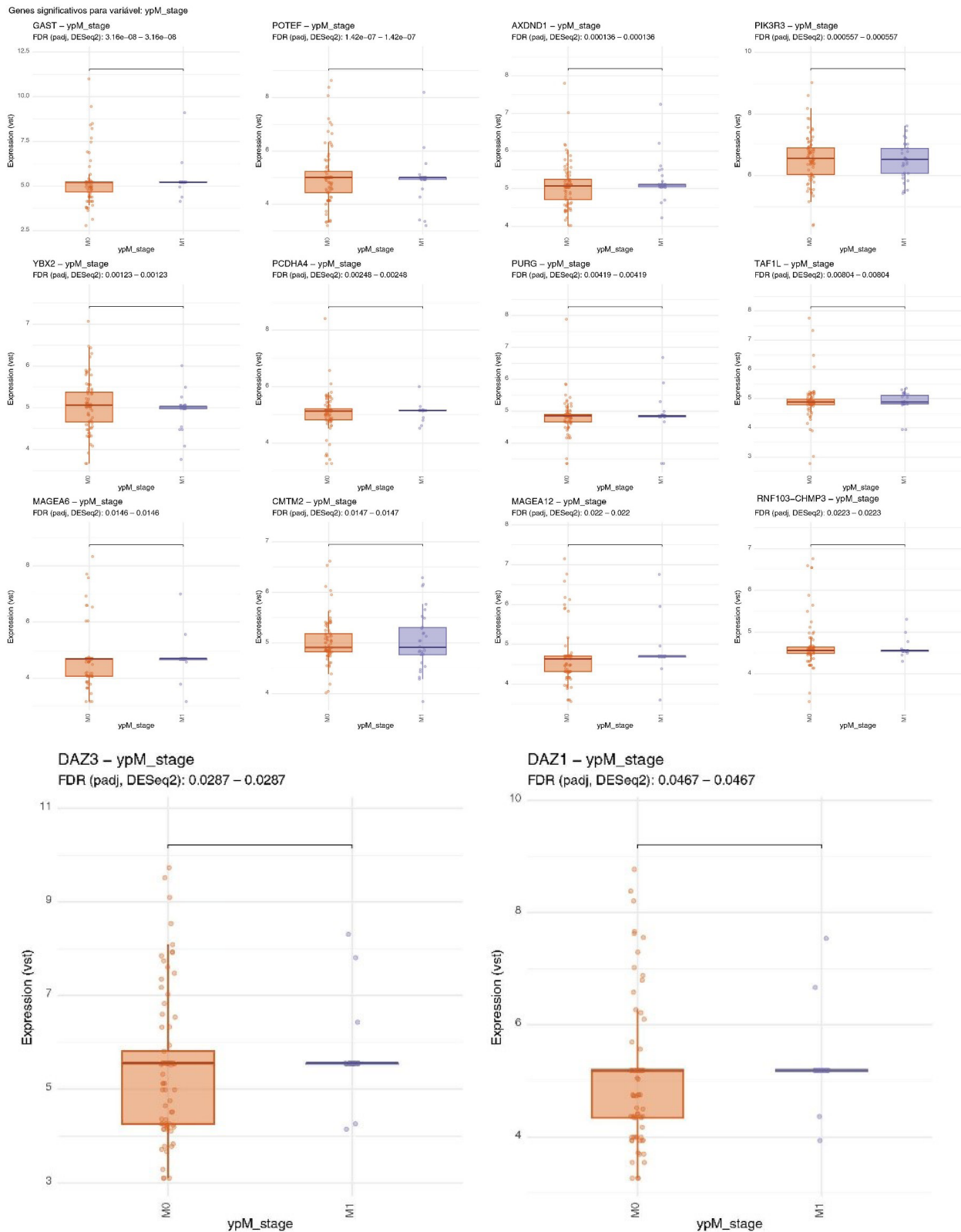
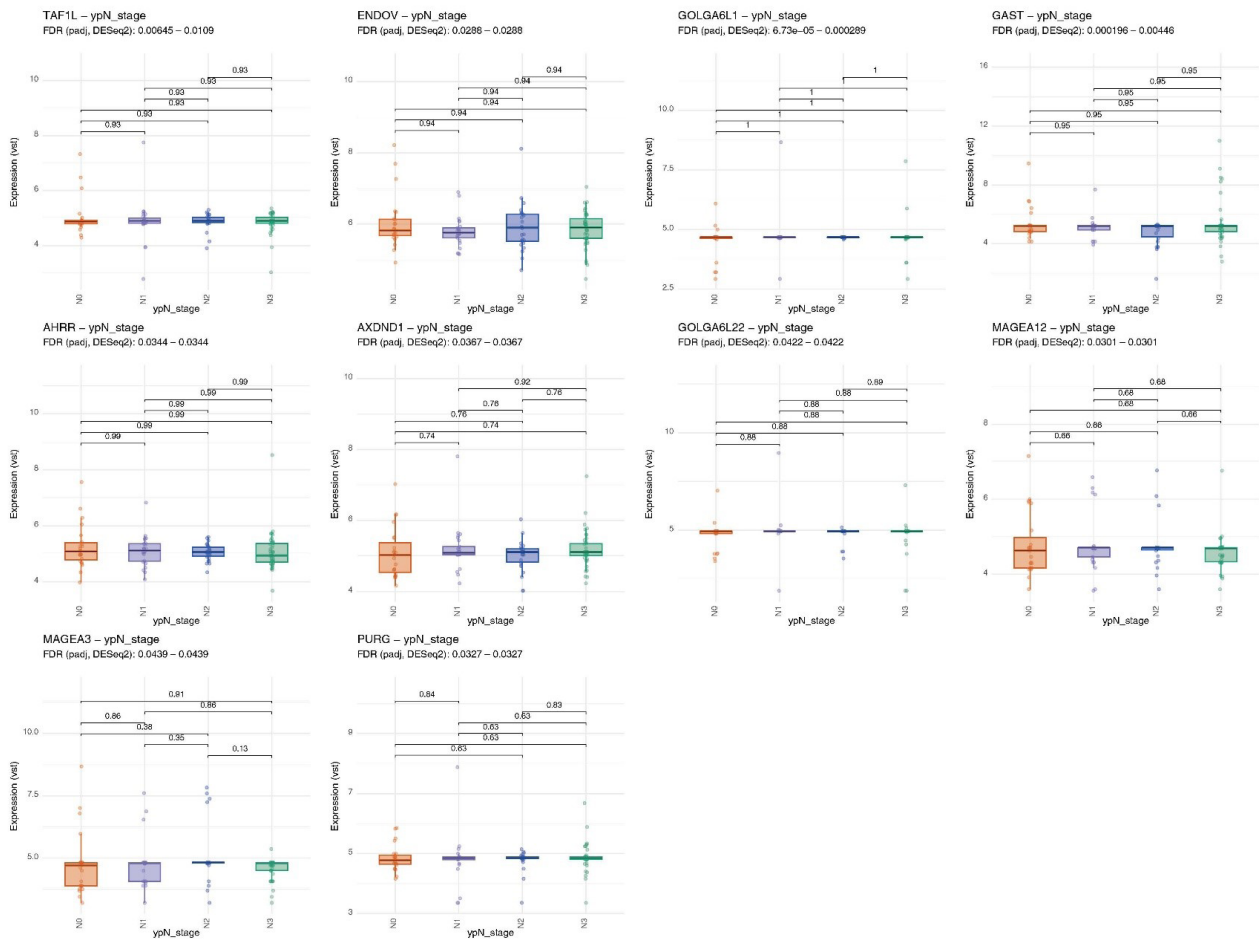


Figure S1. Continued

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**Figure S1.** Association between gene expression and clinical variables. Boxplots represent variance-stabilized expression levels of selected genes across clinical categories, including cTNM stage, gender, Lauren classification, T stage, ypM stage, ypN stage, and therapeutic management. Statistically significant differences between groups are indicated by adjusted *p*-values (FDR; DESeq2).

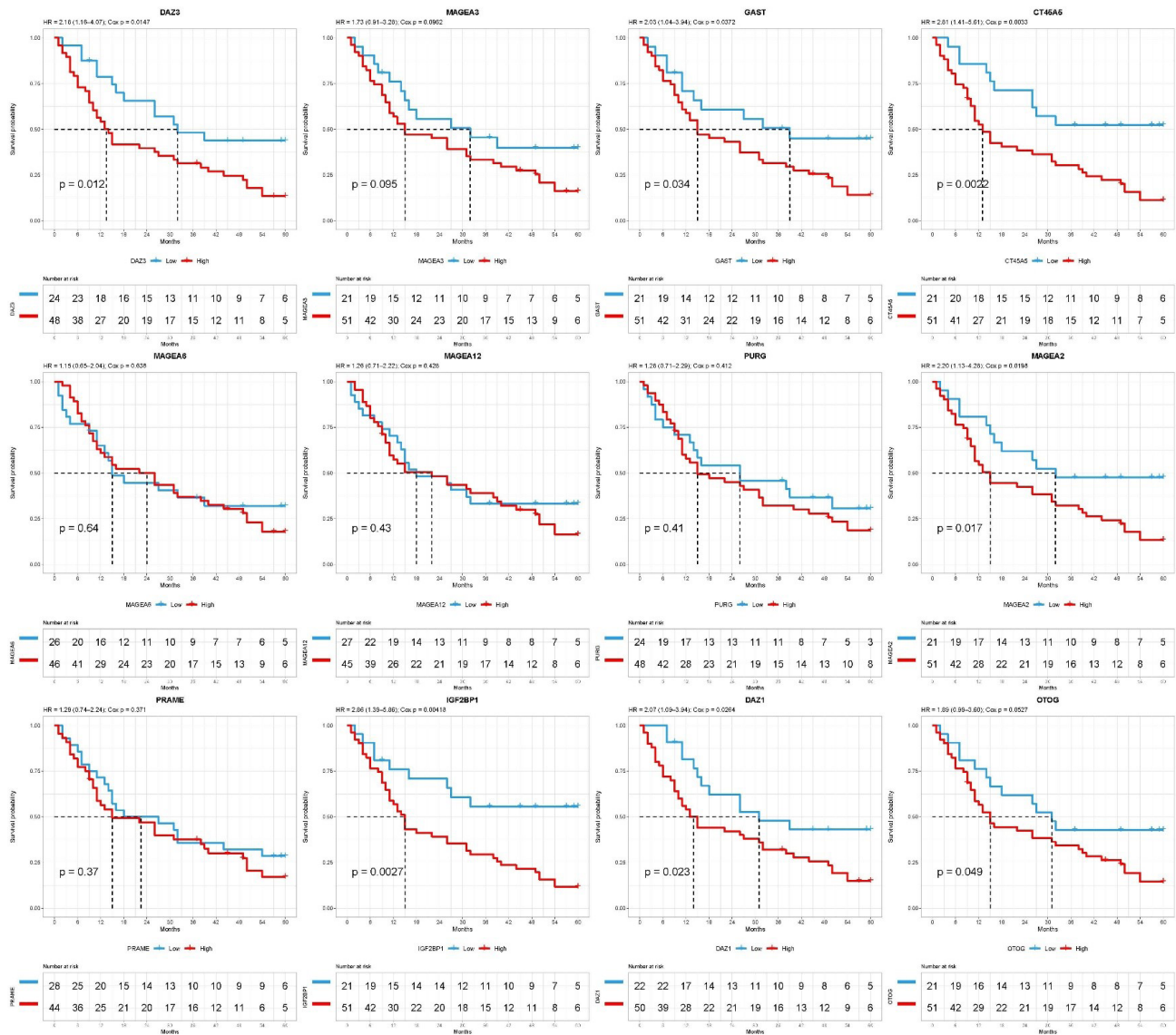


Figure S2. Continued

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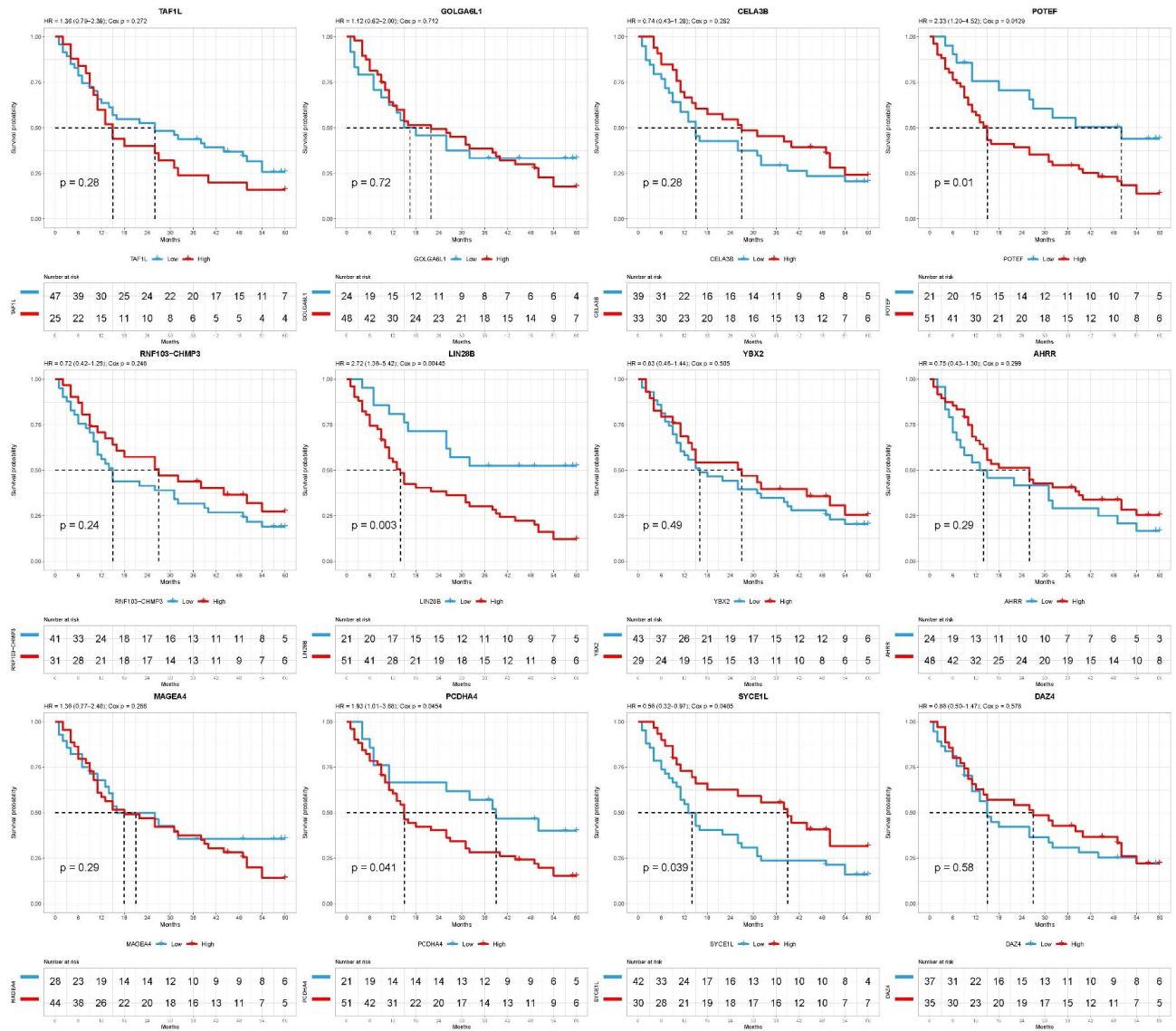


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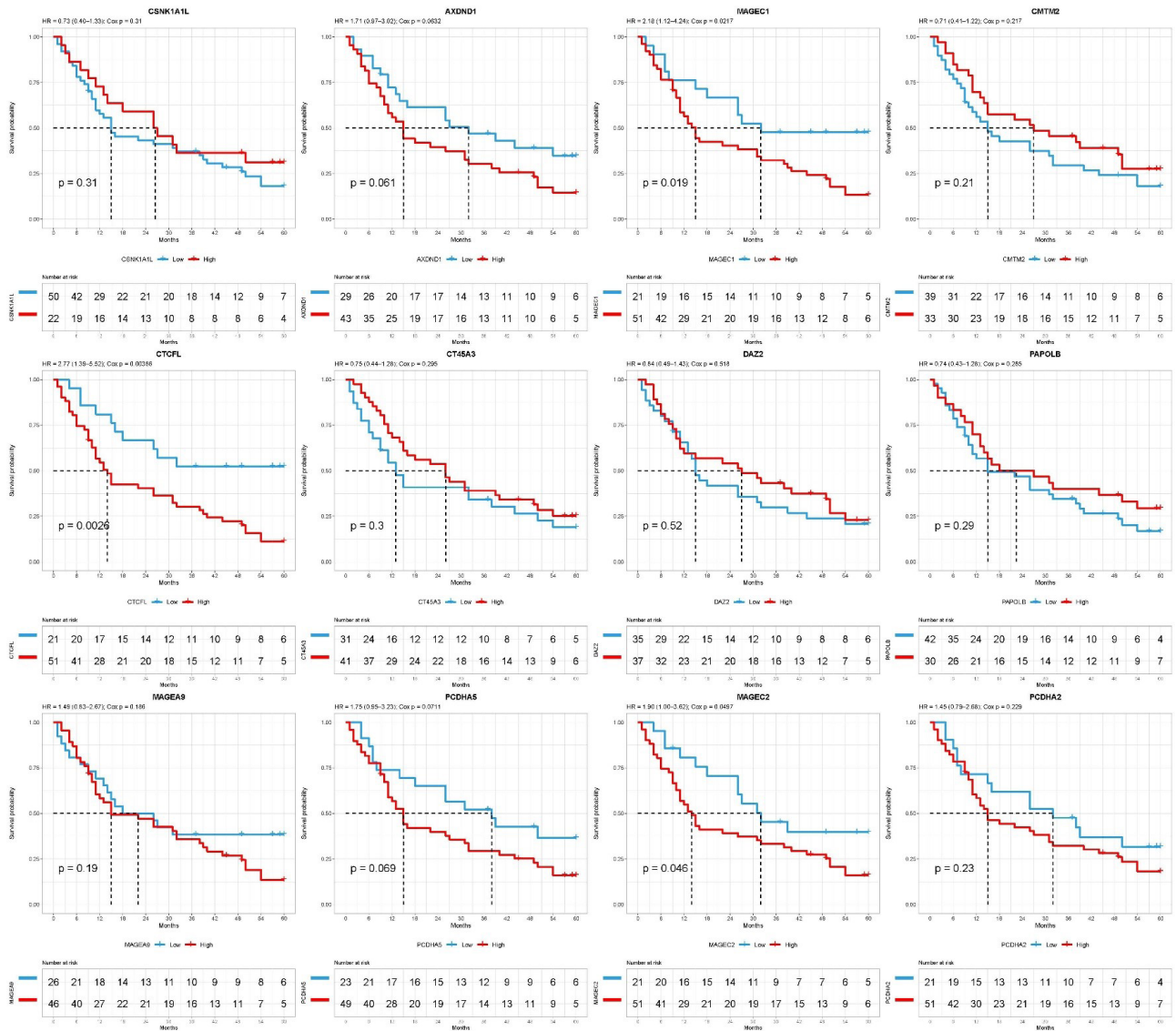


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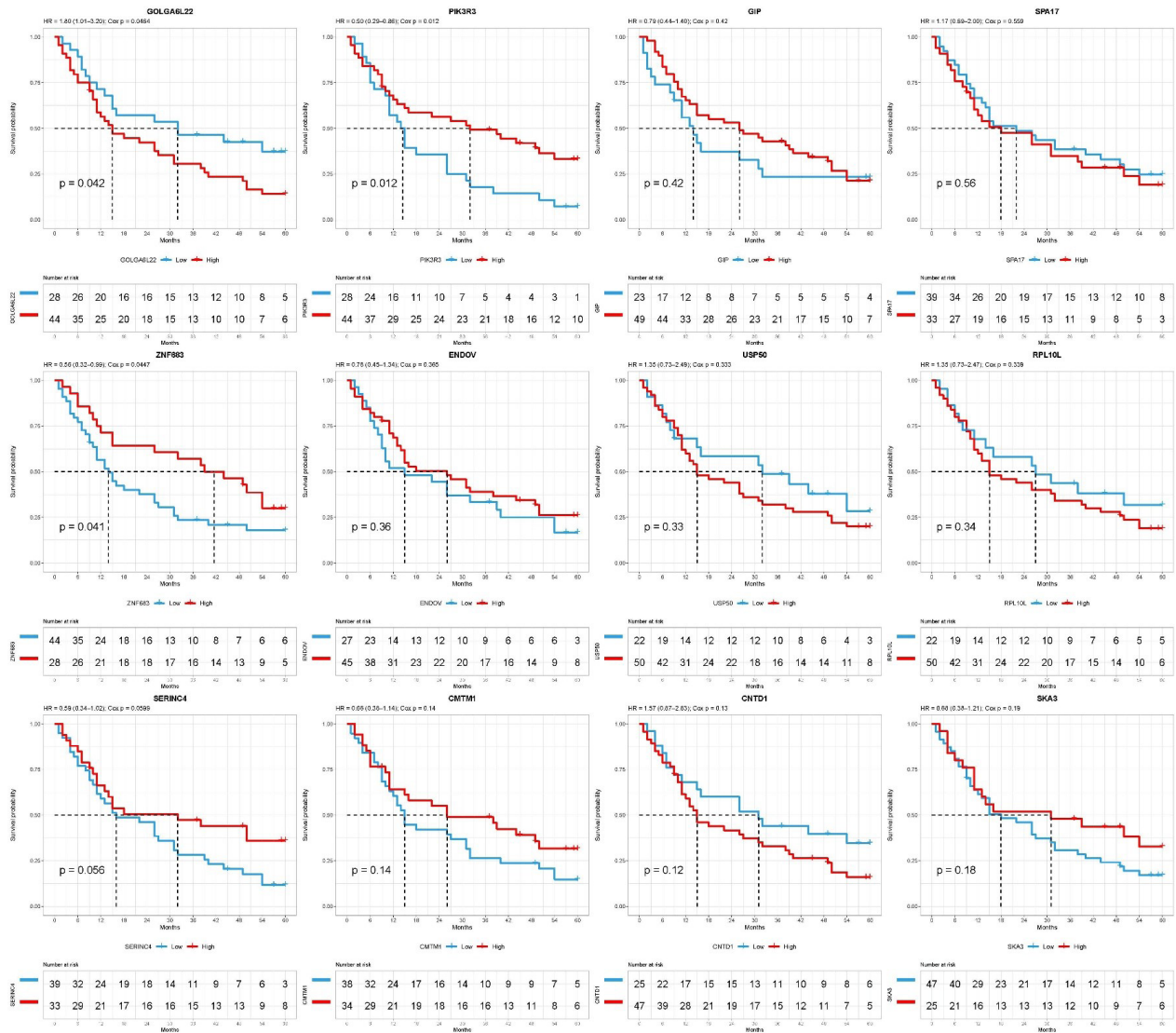
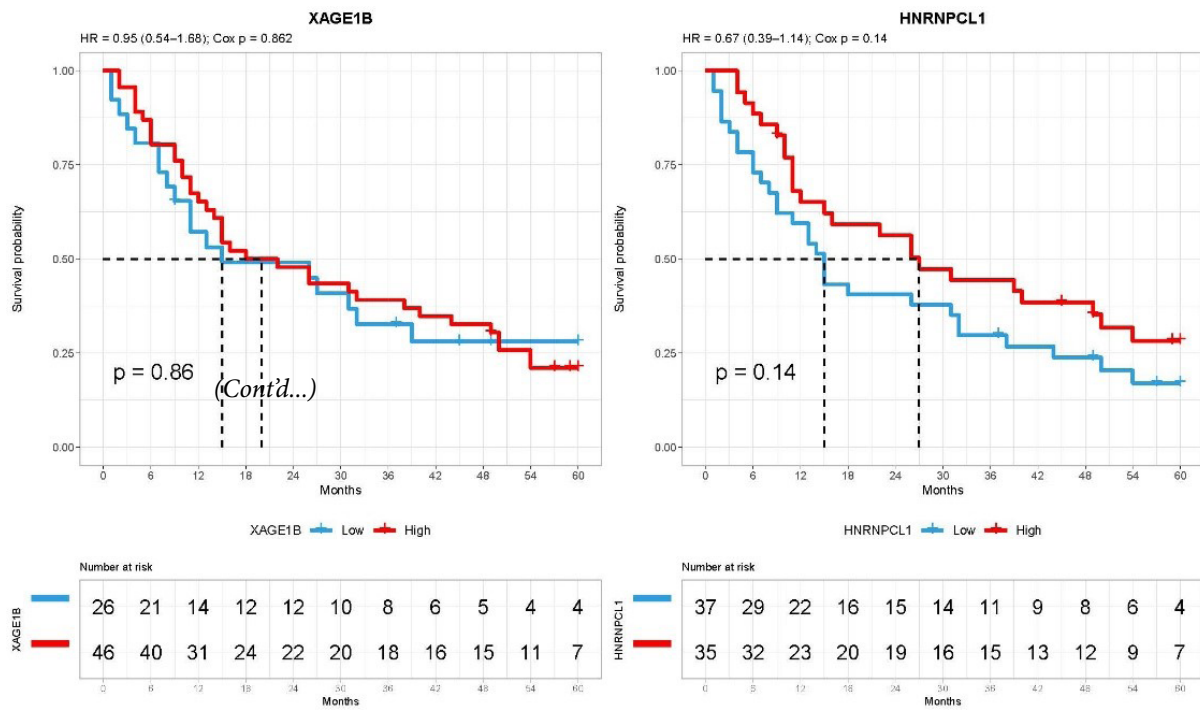


Figure S2. Continued

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**Figure S2.** Survival analysis based on gene expression levels. Kaplan–Meier survival curves show overall survival (OS) according to high and low expression levels of multiple genes. Patients were stratified by gene expression level, and survival differences between groups were assessed using the log-rank test. Hazard ratios (HRs) with 95% confidence intervals and *p*-values from Cox proportional hazards models are indicated.